

1 GGCCTAATCT GCTGCTTGCA AACAAAAAA CCACCGCTAC CAGCGGTGGT  
51 TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GAACTGGCTT  
101 CAGCAGAGCG CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG  
151 GCCACCACTT CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA  
201 ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG  
251 GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA  
301 CGGGGGGTTC GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA  
351 CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC TTCCCGAAGG  
401 GAGAAAGGCG GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC  
451 GCACGAGGGA GCTTCCAGGG GGAAACGCCT GGTATCTTTA TAGTCTGTG  
501 GGGTTTCGCC ACCTCTGACT TGAGCGTCGA TTTTGTGAT GCTCGTCAGG  
551 GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCCGAATTA CCGCGGTCTT  
601 TCTCAACGTA AACTTTTACA GCGGCGCGTC ATTTGATATG ATGCGCCCCG  
651 CTTCCCGATA AGGGAGCAGG CCAGTAAAAG CATTACCCGT GGTGGGGTTC  
701 CCGAGCGGCC AAAGGGAGCA GACTCTAAAT CTGCCGTCAT CGACTTCGAA  
751 GGTTCGAATC CTTCCCCCAC CACCATCACT TTCAAAAGTC CGAAAGAATC  
801 TGCTCCCTGC TTGTGTGTG GAGGTCGCTG AGTAGTGGC GAGTAAAT  
851 TAAGCTACAA CAAGGCAAGG CTTGACCGAC AATTGCATGA AGAATCTGCT  
901 TAGGGTTAGG CGTTTTGCGC TGCTTCGCGA TGTACGGGCC AGATATACGC  
951 GTTGACATTG ATTATTGACT AGTTATTAAT AGTAATCAAT TACGGGGTCA  
1001 TTAGTTCATA GCCCATATAT GGAGTTCGCG GTTACATAAC TTACGGTAA  
1051 TGGCCCCGCT GGCTGACCGC CCAACGACCC CGGCCATTG ACGTCAATAA  
1101 TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA  
1151 TGGGTGGACT ATTTACGGTA AACTGCCCAC TTGGCAGTAC ATCAAGTGTA  
1201 TCATATGCCA AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCC  
1251 CCTGGCATTG TGCCAGTAC ATGACCTTAT GGGACTTTCC TACTTGGCAG  
1301 TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGATGC GGTTTTGGCA  
1351 GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGA TTTCCAAGTC  
1401 TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGACCA AAATCAACGG  
1451 GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG  
1501 AATTCCTGGG CGGGACTGGG GAGTGGCGAG CCCTCAGATG CTGCATATAA  
1551 GCAGCTGCTT TTTGCCTGTA CTGGGTCTCT CTGGTTAGAC CAGATCTGAG  
1601 CCTGGGAGCT CTCTGGCTAA CTAGAGAACC CACTGCTTAA GCCTCAATAA  
1651 AGCTTCTAGA GATCCCTCGA CCTCGAGGGA TCTCCATAC CTACCAGTTC

FIG. 1-1

0936544.041701

1701 TGGCGCTGCA GGTGCGGGCC GCGACTCTAG AGGATCTTTG TGAAGGAACC  
1751 TTACTTCTGT GGTGTGACAT AATTGGACAA ACTACCTACA GAGATTTAAA  
1801 GCTCTAAGGT AAATATAAAA TTTTAAAGTG TATAATGTGT TAACTACTG  
1851 ATTCTAATTG TTTGTGTATT TTAGATTCCA ACCTATGGAA CTGATGAATG  
1901 GGAGCAGTGG TGAATGCCT TTAATGAGGA AAACCTGTTT TGCTCAGAAG  
1951 AAATGCCATC TAGTGATGAT GAGGCTACTG CTGACTCTCA ACATTCTACT  
2001 CCTCCAAAAA AGAAGAGAAA GGTAGAAGAC CCCAAGGACT TTCCTTCAGA  
2051 ATTGCTAAGT TTTTGAGTC ATGCTGTGTT TAGTAATAGA ACTCTTGCTT  
2101 GCTTTGCTAT TTACACCACA AAGGAAAAAG CTGCACTGCT ATACAAGAAA  
2151 ATTATGGAAA AATATTCTGT AACCTTTATA AGTAGGCATA ACAGTTATAA  
2201 TCATAACATA CTGTTTTTTC TTAACCACA CAGGCATAGA GTGTCTGCTA  
2251 TTAATAACTA TGCTCAAAAA TTGTGTACCT TTAGCTTTTT AATTGTAA  
2301 GGGGTTAATA AGGAATATTT GATGTATAGT GCCTTGACTA GAGATCATAA  
2351 TCAGCCATAC CACATTTGTA GAGGTTTTAC TTGCTTTAAA AAACCTCCCA  
2401 CACCTCCCC TGAACCTGAA ACATAAAATG AATGCAATTG TTGTTGTTAA  
2451 CTTGTTTATT GCAGCTTATA ATGGTTACAA ATAAAGCAAT AGCATCACAA  
2501 ATTTACAAA TAAAGCATTT TTTTCACTGC ATTCTAGTTG TGGTTTGTCC  
2551 AAACATCA ATGTATCTTA TCATGTCTGG ATCCTGTGGA ATGTGTGTCA  
2601 GTTAGGGTGT GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA AGTATGCAAA  
2651 GCATGCATCT CAATTAGTCA GCAACCAGGT GTGGAAAGTC CCCAGGCTCC  
2701 CCAGCAGGCA GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAT  
2751 AGTCCCGCCC CTAACCTCCG CCATCCCGCC CCTAACCAG CCCAGTCCG  
2801 CCCATTCTCC GCCCCATGGC TGAATAATTT TTTTATTTA TGCAGAGGCC  
2851 GAGGCCGCCT CGGCCTCTGA GCTATTCCAG AAGTAGTGAG GAGGCTTTTT  
2901 TGGAGGCCTA GGCTTTTGCA AAAAGCTAAT TC

FIG. 1-2

CCTAAGATGAGCTTTCCATGTAAATTTGTAGCCAGCTTCCTTCTGATTTTCAATGTTTCT (60)  
 METSERPHEPROCYSLYSPHEVALALASERPHELEULEULEPHEASNVALSER  
 TCCAAAGGTGCAGTCTCCAAAGAGATTACGAATGCCTTGGAAACCTGGGTCCTTGGGT (120)  
 SERLYSGLYALAVALSERLYSGLUILETHRASNALALEUGLUTHRTRPGLYALALEUGLY  
 CAGGACATCAACTTGGACATTCCTAGTTTCAAATGAGTGATGATATTGACGATATAAAA (180)  
 20 GLNASPILEASNLEUASPILEPROSERPHEGLNMETSERASPPASPILEASPPASPILELYS  
 TGGGAAAAAÄCTTCAGACAAGAAAAAGATTGCACAATTCAGAAAAGAGAAAGAGACTTTC (240)  
 40 TRPGLULYSTHRERASPLYSLYSILEALAGLNPHEARGLYSGLULYSGLUTHRPHE  
 AAGGAAAAAGATACATATAAGCTATTTAAATGGAACCTGTGAAAATTAAGCATCTGAAG (300)  
 60 LYSGLULYSASPTHRTRYRLYSLEUPHELYSASNGLYTHRLEULYSILELYSHISLEULYS  
 ---CHO---  
 ACCGATGATCAGGATATCTACAAGGTATCAATATATGATACAAAAGGAAAAATGTGTTG (360)  
 80 THRASPASPGLNASPILEYRLYSVALSERILETYRASPTHRLYSGLYLYSASNVALLEU  
 GAAAAAATAITTTGATTTGAAGATTCAAGAGAGGGTCTCAAAACCAAAGATCTCCTGGACT (420)  
 100 GLULYSILEPHEASPLEULYSILEGLNGLUARGVALSERLYSPROLYSILESERTRPTHR  
 TGTATCAACACAACCTGACCTGTGAGGTAAATGAATGGAÄCTGACCCCGAATTAAACCTG (480)  
 120 CYSILEASNTHRTHRLEUTHRCYSGLUVALMETASNGLYTHRASPPOGLULEUASNLEU  
 ---CHO--- ---CHO---  
 TATCAAGATGGGAAACATCTAAACCTTCTCAGAGGGTCATCACACAAAGTGGACCACC (540)  
 140 TYRGLNASPGLYLYSHISLEULYSLEUSERGLNARGVALILETHRHSLYSTRPTHRTHR  
 AGCCTGAGTGCAAAATTCAGTGACAGCAGGGAACAAAGTCAGCAAGGAATCCAGTGTCT (600)  
 160 SERLEUSERALALYSPELYSCYSTHRALAGLYASNLYSVALSERLYSGLUSERSERVAL  
 GAGCCTGTGAGCTGTCCAGAGAAAGGTCTGGACATCTATCTCATCATTGGCATATGTGGÄ (660)  
 180 GLUPROVALSERCYSPROGLULYSGLYLEUASPILEYRLEUILEILEGLYILECYSGLY  
 GGAGGCAGCCTCTTGATGGTCTTTGTGGCÄCTGCTCGTTTTCTATATCACCAAAGGAAA (720)  
 200 GLYGLYSERLEULEUMETVALPHEVALALALEULEUVALPHETYRILETHRLYSARGLYS  
 -----TM-----  
 AAACAGAGGAGTCGGAGAAATGATGAGGAGCTGGAGACAAGAGCCACAGAGTAGCTACT (780)  
 220 LYSGLNARGSERARGARGASNASPLUGLULEUGLUTHRARGALAHISARGVALALATHR  
 GAAGAAAGGGGCCGGAAGCCCAACAAATTCAGCTTCAÄCCCTCAGAAATCCAGCAACT (840)  
 240 GLUGLUARGGLYARGLYSPROGLNGLNILEPROALASERTHRPROGLNASNPROALATHR  
 TCCCAACATCTCTCCACCACCTGGTCATCGTTCCAGGCACCTAGTCATCGTCCCCCG (900)  
 260 SERGLNHISPROPROPROPROGLYHISARGSERGLNALAPROSERHISARGPROPRO  
 CCTCCTGGAÄCCCGTGTTCAGCACCAGCCTCAGAAGAGGCTCCTGCTCCTCGTGGGCACÄ (960)  
 280 PROPROGLYHISARGVALGLNHISGLNPROGLNLYSARGPROPROALAPROSERGLYTHR

FIG. 2-1

093544-4496

300 CAAGTTCAC<sup>2</sup>CAGCAGAAAG<sup>3</sup>CCCGCCCT<sup>4</sup>CCCCAGACCT<sup>5</sup>CGAGTTCAGC<sup>6</sup>AAAACCTCC<sup>7</sup> (1020)  
GLNVALHISGLNGLNLYSGLYPRO<sup>8</sup>PROLEU<sup>9</sup>PROARG<sup>10</sup>PROARG<sup>11</sup>VALGLN<sup>12</sup>PROLYSPRO<sup>13</sup>PRO  
320 CATGGGGCAGCAGAAA<sup>14</sup>ACT<sup>15</sup>CATTGTCCCCT<sup>16</sup>CCTCTAATT<sup>17</sup>AAAAAAGAT<sup>18</sup>AGAAACTGTCT<sup>19</sup> (1080)  
HISGLYALA<sup>20</sup>LAGLUASN<sup>21</sup>SERLEU<sup>22</sup>SERPRO<sup>23</sup>SER<sup>24</sup>SERASN<sup>25</sup>END  
TTTTCAATA<sup>26</sup>AAAAGCACTGT<sup>27</sup>GGATTTCTG<sup>28</sup>CCCTCCTGATGTGCATATCCG<sup>29</sup>TACTTCCATG<sup>30</sup> (1140)  
AGGTGTTTTCTGTGTGCAG<sup>31</sup>AACATTGTCA<sup>32</sup>CTCCTGAGGCTGTGGGCA<sup>33</sup>CAGCCACCTCT<sup>34</sup> (1200)  
GCATCTTCGA<sup>35</sup>ACTCAGCCA<sup>36</sup>TGTGGTCAAC<sup>37</sup>ATCTGGAGTTTTGGTCTCCT<sup>38</sup>CAGAGAGCTC<sup>39</sup> (1260)  
CATCACACCAGTAAGGAGAAGCAATATAAGTGTGATTGCAAGAATGGTAGAGGACCGAGC<sup>40</sup> (1320)  
ACAGAAATCTTAGAGATTTCTTGTCCCCTCTCAGGTCATGTGTAGATGCCGATAAATCAAG<sup>41</sup> (1380)  
TGATTGGTGTGCCTGGGTCTCACTACAAGCAGCCTATCTGCTTAAGAGACTCTGGAGTTT<sup>42</sup> (1440)  
CTTATGTGCCCTGGTGGACACTTGCCCA<sup>43</sup>CCATCCTGTGAGTAAAAGTGA<sup>44</sup>AATAAAGCTT<sup>45</sup> (1500)  
TGAC (1504)

FIG. 2-2

1 G C C C G A G C C A T G G T T G C T G G G A G C G A C G C G G G G C C C T G G G G T C C T C A G C G T G G T C I G C C T G C T G C A C T G C T T T G G T T T C A T C 90  
MetValAlaGlySerAspAlaGlyArgAlaLeuGlyValLeuSerValValCysLeuLeuHisCysPheGlyPheIle 26

91 A G C T G T T T T C C C A A C A A A T A T A T G G T G T G T A T G G G A A T G T A A C T T T C C A T G T A C C A A G C A A T G T G C C T T T A A A A G A G G T C C T A T G G 180  
27 SerCysPheSerGlnGlnIleTyrGlyValValTyrGlyAsnValThrPheHisValProSerAsnValProLeuLysGluValLeuTrp 56  
---CH0---

181 A A A A A C A A A A G C A T A A A G T T G C A G A A C T G G A A A T T C T G A A T T C A G A G C T T T C T C A T C T T T A A A A A T A G G G T T T A T T T A G A C A C I G T G 270  
57 LysLysGlnLysAspLysValAlaGluLeuGluAsnSerGluPheArgAlaPheSerSerPheLysAsnArgValTyrLeuAspThrVal 86

271 T C A G G T A G C C T C A C I A T C T A C A A C T T A A C A T C A T C A G A T G A G A T G A G T A T G A A T G G A A T C G C C A A A T A T T A C T G A T A C C A T G A A G T T C 360  
87 SerGlySerLeuThrIleTyrAsnLeuThrSerSerAspGluAspGluTyrGluMetGluSerProAsnIleThrAspThrMetLysPhe 116  
---CH0---

361 T T T C T T T A T G T G A G T C T C T C C A T C T C C C A C A C T A A C T T G T G C A T T G A C T A A T G G A A G C A T T G A A G T C C A A T G C A T G A T A C C A G A G 450  
117 PheLeuTyrValLeuGluSerLeuProSerProThrLeuThrCysAlaLeuThrAsnGlySerIleGluValGlnCysMetIleProGlu 146  
---CH0---

451 C A T T A C A A C A G C C A T C G A G G A C T T A T A A T G T A C T C A T G G G A T T G T C C T A T G G A G C A A T G T A A C G T A A C T C A A C C A G T A T A T A T T T A A G 540  
147 HisTyrAsnSerHisArgGlyLeuIleMetTyrSerTrpAspCysProMetGluGlnCysLysArgAsnSerThrSerIleTyrPheLys 176  
---CH0---

541 A T G G A A A T G A T C T T C C A C A A A A A A T A C A G T G T A C T C T T A G C A A T C C A T T A T T A A T A C A A C A C A T C A T C A A T C A T T T T G A C A A C C T G T A T C 630  
177 MetGluAsnAspLeuProGlnLysIleGlnCysThrLeuSerAsnProLeuPheAsnThrThrSerSerIleIleLeuThrThrCysIle 206  
---CH0---

631 C C A A G C A G C G G T C A T T C A A G A C A C A G A T A T G C A C T T A T A C C C A T A C C A T T A G C A G T A A T T A C A A C A T G T A T T G T G T G T A T A T A T A G A A T G T T 720  
207 ProSerSerGlyHisSerArgHisArgTyrAlaLeuIleProIleProLeuAlaValIleThrThrCysIleValLeuTyrMetAsnVal 236  
=====

721 C T T T A A T T G A G A G A C A A T T C T T C A T T T T A G G T A T T C T G A A A T G T G A C A G A A A C C A G A C A G A C C A A C T C C A A T T G A T T G G T A A C A G 810  
237 LeuEnd  
===

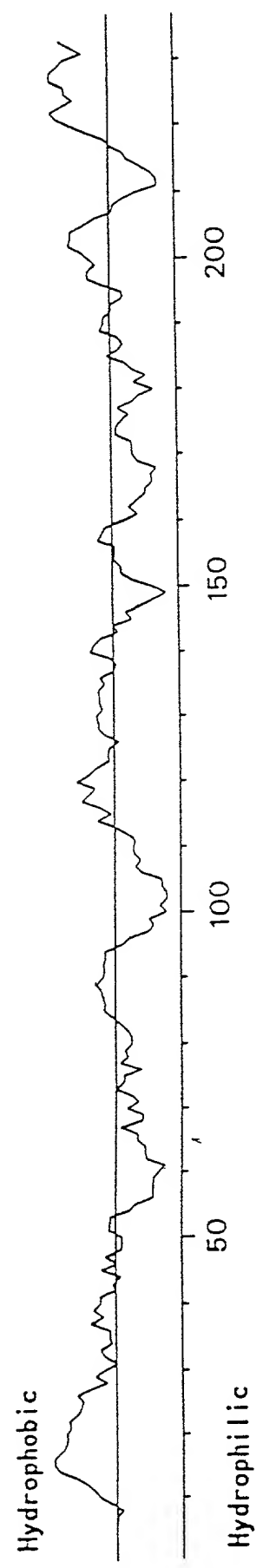
811 A A G A T G A A G A C A A C A G C A T A A C T A A A T A T T T A A A A A C T A A A A G C C A T C T G A T T T C T C A T T 874

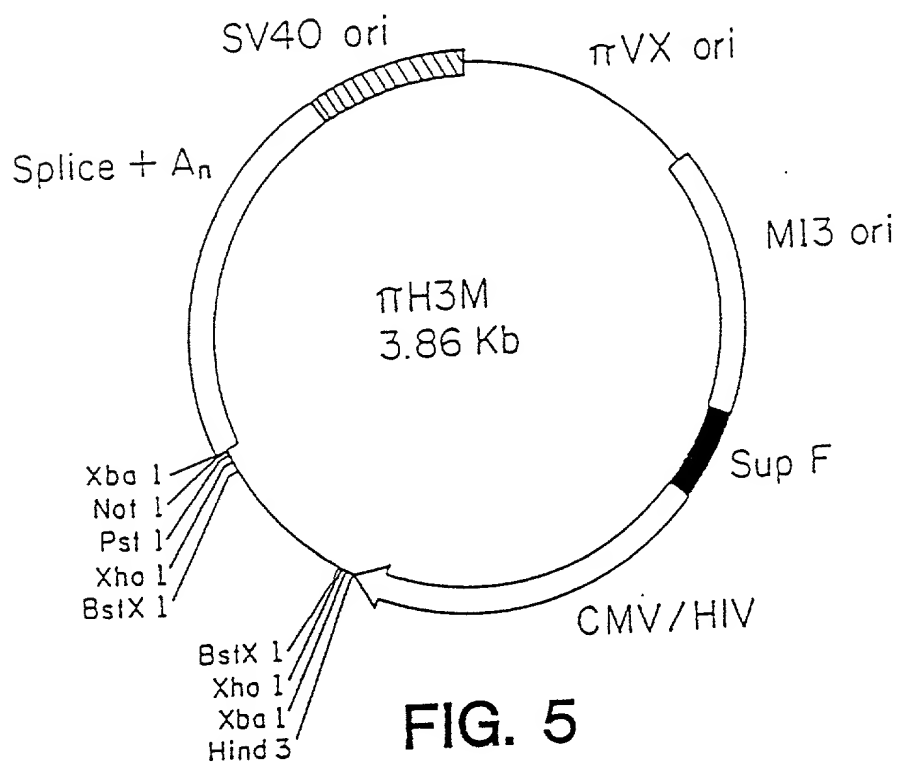
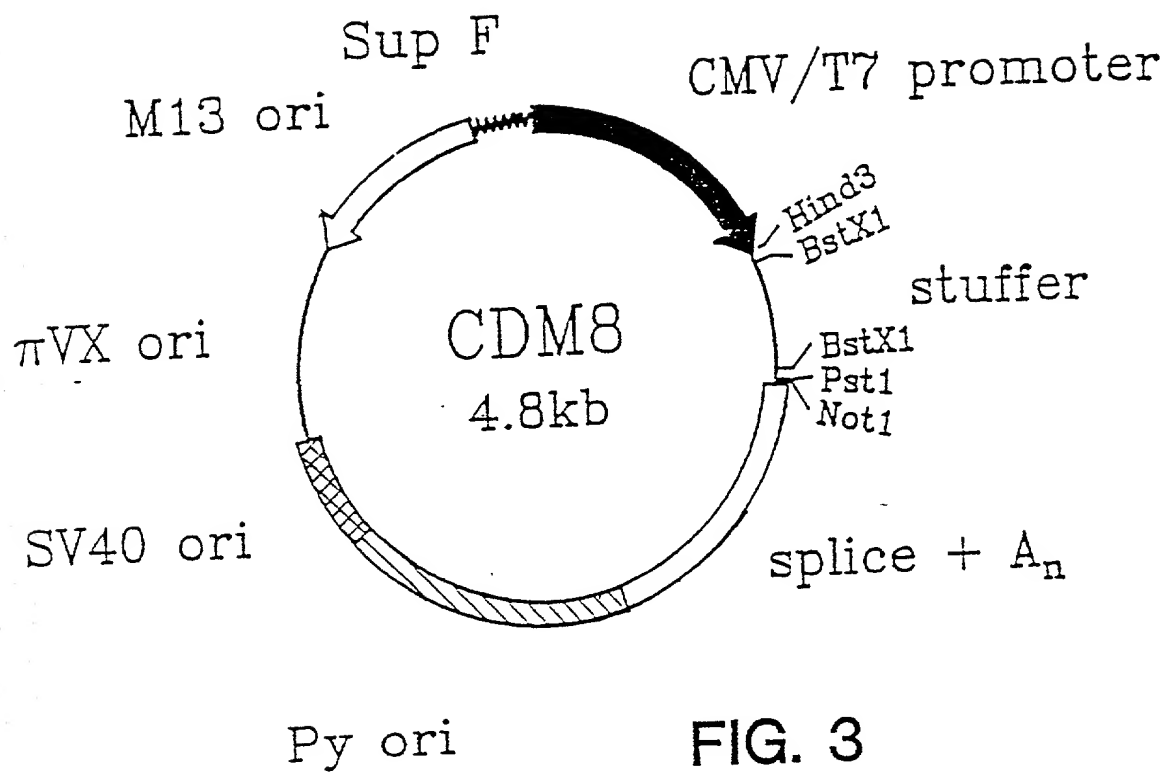
FIG. 4A

237 LouEnd

811 AGATGAAGACAACAGCATAACTAAATTATTTTAAAACTAAAAAGCCATCTGATTTCTCATTT 874

FIG. 4B





1 GCGTAATCT GCTGCTTGCA AACAAAAAA CCACCGCTAC CAGCGGTGGT  
 51 TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAAGTGGCT  
 101 TCAGCAGAGC GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA  
 151 GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT  
 201 AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG  
 251 GGTGGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA  
 301 ACGGGGGGTT CGTGACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA  
 351 ACTGAGATAC CTACAGCGTG AGCATTGAGA AAGCGCCACG CTTCCCGAAG  
 401 GGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG  
 451 CGCAGGAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGTCTGT  
 501 CCGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTGTGA TGCTCGTCAG  
 551 GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCAAGCTA GCTTCTAGCT  
 601 AGAAATTGTA AACGTTAATA TTTTGTTAAA ATTCGCGTTA AATTTTTGTT  
 651 AAATCAGCTC ATTTTTTAAC CAATAGGCCG AAATCGGCAA AATCCCTTAT  
 701 AAATCAAAAG AATAGCCCGA GATAGGGTTG AGTGTGTTC CAGTTTGGA  
 751 CAAGAGTCCA CTATTAAAGA ACGTGGACTC CAACGTCAA GGGCGAAAAA  
 801 CCGTCTATCA GGGCGATGGC CGCCCACTAC GTGAACCATC ACCCAAATCA  
 851 AGTTTTTTGG GGTGAGGTG CCGTAAAGCA CTAAATCGGA ACCCTAAAGG  
 901 GAGCCCCCGA TTTAGAGCTT GACGGGGAAA GCCGGCGAAC GTGGCGAGAA  
 951 AGGAAGGGAA GAAAGCGAAA GGAGCGGGCG CTAGGGCGCT GGCAAGTGTA  
 1001 GCGGTCACGC TGGCGTAAC CACCACACC GCCGCGCTTA ATGCGCGCT  
 1051 ACAGGGCGCG TACTATGGTT GCTTTGACGA GCACGTATAA CGTGCTTTCC

FIG. 6-1



1101 TCGTTGGAAT CAGAGCGGGA GCTAAACAGG AGGCCGATTA AAGGGATTTT  
 1151 AGACAGGAAC GGTACGCCAG CTGGATCACC GCGGTCTTTC TCAACGTAAC  
 1201 ACTTTACAGC GCGCGTCAT TTGATATGAT GCGCCCCGCT TCCCGATAAG  
 1251 GGAGCAGGCC AGTAAAAGCA TTACCCGTGG TGGGGTCCC GAGCGGCCAA  
 1301 AGGGAGCAGA CTCTAAATCT GCCGTCATCG ACTTCGAAGG TTCGAATCCT  
 1351 TCCCCACCA CCATCACTTT CAAAAGTCCG AAAGAATCTG CTCCCTGCTT  
 1401 GTGTGTTGGA GGTGCTGAG TAGTGCGCGA GTAAAATTTA AGCTACAACA  
 1451 AGGCAAGGCT TGACCGACAA TTGCATGAAG AATCTGCTTA GGGTTAGGCG  
 1501 TTTTGGCTG CTTCGCGATG TACGGGCCAG ATATACGCGT TGACATTGAT  
 1551 TATTGACTAG TTATTAATAG TAATCAATTA CGGGGTCATT AGTTCATAGC  
 1601 CCATATATGG AGTTCGCGT TACATAACTT ACGGTAAATG GCCCCCTGG  
 1651 CTGACCGCCC AACGACCCCC GCCCATTGAC GTCAATAATG ACGTATGTTT  
 1701 CCATAGTAAC GCCAATAGGG ACTTTCCATT GACGTCAATG GGTGGACTAT  
 1751 TTACGGTAA\* CTGCCCCACTT GGCAGTACAT CAAGTGATC ATATGCCAAG  
 1801 TACGCCCCCT ATTGACGTCA ATGACGGTAA ATGGCCCGCC TGGCATTATG  
 1851 CCCAGTACAT GACCTTATGG GACTTTCCTA CTTGGCAGTA CATCTACGTA  
 1901 TTAGTCATCG CTATTACCAT GGTGATGCGG TTTTGGCAGT ACATCAATGG  
 1951 GCGTGGATAG CGGTTTGA CT CACGGGGATT TCCAAGTCTC CACCCCATTG  
 2001 ACGTCAATGG GAGTTTGT TT TGGCACCAA ATCAACGGGA CTTTCCAAAA  
 2051 TGTGTAACA ACTCCGCCCC ATTGACGCAA ATGGGCGGAA TTCCTGGGCG  
 2101 GGA CTGGGGA GTGGCGAGCC CTCAGATGCT GCATATAAGC AGCTGCTTTT  
 2151 TGCCTGTA CT GGGTCTCTCT GGTTAGACCA GATCTGAGCC TGGGAGCTCT  
 2201 CTGGCTAACT AGAGAACCCA CTGCTTAAGC CTCAATAAAG CTTCTAGAGA  
 2251 TCCCTCGACC TCGAGATCCA TTGTGCTGGC GCGGATTCTT TATCACTGAT

FIG. 6-2

2301 AAGTTGGTGG ACATATTATG TTTATCAGTG ATAAAGTGTC AAGCATGACA  
 2351 AAGTTGCAGC CGAATACAGT GATCCGTGCC GCCCTAGACC TGTGAACGA  
 2401 GGTGCGCGTA GACGGTCTGA CGACACGCAA ACTGGCGGAA CGGTTGGGGG  
 2451 TTCAGCAGCC GGCCTTTTAC TGGCACTTCA GGAACAAGCG GGCCTGCTC  
 2501 GACGCACTGG CCGAAGCCAT GCTGGCGGAG AATCATAGCA CTTCGGTGCC  
 2551 GAGAGCCGAC GACGACTGGC GCTCATTCT GACTGGGAAT GCGCGCAGCT  
 2601 TCAGGCAGGC GCTGCTCGCC TACCGCCAGC ACAATGGATC TCGAGGGATC  
 2651 TTCCATACCT ACCAGTTCTG CGCCTGCAGG TCGCGGCCGC GACTCTAGAG  
 2701 GATCTTTGTG AAGGAACCTT ACTTCTGTGG TGTGACATAA TTGGACAAAC  
 2751 TACCTACAGA GATTTAAAGC TCTAAGGTAA ATATAAAATT TTTAAGTGTA  
 2801 TAATGTGTTA AACTACTGAT TCTAATTGTT TGTGTATTTT AGATTCCAAC  
 2851 CTATGGAACCT GATGAATGGG AGCAGTGGTG GAATGCCTTT AATGAGGAAA  
 2901 ACCTGTTTTG CTCAGAAGAA ATGCCATCTA GTGATGATGA GGCTACTGCT  
 2951 GACTCTCAAC ATTCTACTCC TCCAAAAAAG AAGAGAAAGG TAGAAGACCC  
 3001 CAAGGACTTT CCTTCAGAAT TGCTAAGTTT TTTGAGTCAT GCTGTGTTTA  
 3051 GTAATAGAAC TCTTGCTTGC TTTGCTATTT ACACCACAAA GGAAAAAGCT  
 3101 GCACTGCTAT ACAAGAAAAT TATGGAAAAA TATTCTGTAA CCTTTATAAG  
 3151 TAGGCATAAC AGTTATAATC ATAACATACT GTTTTTTCTT ACTCCACACA  
 3201 GGCATAGAGT GTCTGCTATT AATAACTATG CTCAAAAATT GTGTACCTTT  
 3251 AGCTTTTTTAA TTTGTAAAGG GGTAAATAAG GAATATTTGA TGTATAGTGC  
 3301 CTTGACTAGA GATCATAATC AGCCATACCA CATTTGTAGA GGTTTTACTT  
 3351 GCTTTAAAAA ACCTCCCACA CCTCCCCCTG AACCTGAAAC ATAAAATGAA  
 3401 TGCAATTGTT GTTGTTAACT TGTATTATGC AGCTTATAAT GGTTACAAAT  
 3451 AAAGCAATAG CATCACAAAT TTCACAAATA AAGCATTTTT TCACTGCAT

**FIG. 6-3**

3501 TCTAGTTGTG GTTTGTCCAA ACTCATCAAT GTATCTTATC ATGTCTGGAT  
3551 CCTGTGGAAT GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG  
3601 CAGGCAGAAG TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAGGTGT  
3651 GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT  
3701 CAATTAGTCA GCAACCATAG TCCCGCCCCT AACTCCGCCC ATCCCGCCCC  
3751 TAACTCCGCC CAGTTCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT  
3801 TTTATTTATG CAGAGGCCGA GGCCGCCTCG GCCTCTGAGC TATTCCAGAA  
3851 GTAGTGAGGA GGCTTTTTTG GAGGCCTAGG CTTTIGCAAA AAGCTAATTC

**FIG. 6-4**

AGACTCTCAGGCTTGGCAGGTGCGTCTTTCAGTTCGCCCTCACACTTCGGGTCTCTCGGG (60)

GAGGAGGGGCTGGAACCTAGCCCATCGTCAGGACAAAGATGCTCAGGCTGCTCTTGGCT (120)

METLEUARGLEULEULEUALA  
-18  
CTCAACTTAITCCCTTCAATTCAAGTAACAGGAAACAAGATTTTGGTGAAGCAGTCGCCC (180)

LEUASNLEUPHEPROSERILEGLNVALTHRGLYASNLYSILELEUVALLYSGLNSERPRO  
+1  
ATGCTTGTAAGCTACGACAATGCGGTCAACCTTAGCTGCAAGTATTCCTACAATCTCTT (240)

METLEUVALALATYRASPASNALAVALASNLEUSERCYSLYSTYRSERTYRASNLEUPHE  
---CHO---  
TCAAGGGAGITCCGGGCATCCCTTCACAAAGGACTGGATAGTGCTGTGGAGTCTGTGT (300)

SERARGGLUPHEARGALASERLEUHSLSYGLYLEUASPSEALAVAGLUVALCYSVAL  
30  
GTATATGGGAATTACTCCCAGCAGCTTCAGGTITACTCAAAAACGGGGTCAACTGTGAT (360)

VALTYRGLYASNLYRSERGLNGLNLEUGLNVALTYRSERLYSTHRGLYPHEASNCYSASP  
---CHO---  
GGGAAATTGGGCAATGAATCAGTGACATTCTACCTCCAGAAATTTGTATGITAACCAAACA (420)

GLYLYSLEUGLYASNGLUSERVALTHRPHETYLEUGLNASNLEUTYRVALASNGLNTHR  
---CHO---  
GATATTTACTTCTGCAAAATTGAAGTTATGTATCCTCCTCCTTACCTAGACAATGAGAAG (480)

ASPILETYRPHECYSLYSILEGLUVALMETTYRPROPROPROTYRLEUASPASNGLULYS  
90  
AGCAATGGAACCATTATCCATGTGAAAGGGAAACACCTTTGTCCAAGTCCCCTATTTCCC (540)

SERASNGLYTHRILEILEHISVALLYSGLYLYSHISLEUCYSPROSERPROLEUPHEPRO  
---CHO---  
GGACCTTCTAAGCCCTTTTGGGTGCTGGTGGTGGTGGTGGAGTCCTGGCTTGCTATAGC (600)

GLYPROSERLYSPROPHETRPVALLEUVALVALVALGLYGLYVALLEUALACYSTYRSER  
130  
-----TM-----  
TTGCTAGTAACAGTGGCCTTTATTATTTTCTGGGTGAGGAGTAAGAGGAGCAGGCTCCTG (660)

LEULEUVALTHRVALALAPHEILEILEPHETRPVALARGSERLYSARGSERARGLEULEU  
150  
CACAGTGACTACATGAACATGACTCCCCGCCGCCCGGGCCACCCGCAAGCATTACCAAG (720)

HISSERASPTYRMETASNMETTHRPROARGARGPROGLYPROTHRARGLYSHISTYRGLN  
170  
CCCTATGCCCCACCACGCGACTTCGCAGCCTATCGCTCCTGACACGGACGCCTATCCAGA (780)

PROTYRALAPROPROARGASPPHEALAALATYRARGSEREND  
190  
AGCCAGCCGGCTGGCAGCCCCATCTGCTCAATATCACTGCTCTGGATAGGAAATGACC (840)

CCATCTCCAGCCGGCCACCTCAGCCCTGTGGGCCACCATGCCAATTTTCTCGAGTG (900)

ACTAGACCAATATCAAGATCATTTTGAGACTCTGAAATGAAGTAAAGAGATTTCTGT (960)

GACAGGCCAAGTCTTACAGTGCCATGGCCACATTCCAACCTACCATGTACTTAGTGACT (1020)

TGACTGAGAAGTTAGGGTAGAAAACAAAAAGGAGTGAATCTGGGAGCCTCTTCCCTTT (1080)

FIG. 7-1

CTCACTCACCTGCACATCTCAGTCAAGCAAAGTGTGGTATCCACAGACATTTTAGTTGCA (1140)  
GAAGAAAGGCTAGGAAATCATTCTTTTGGTTAAATGGGTGTTAATCTTTTGGTTAGTG (1200)  
GGTTAAACGGGTAAGTTAGTAGGGGGAGGGATAGGAAGACATATTTAAAAACCATT (1260)  
AAACACTGTCTCCCACTCATGAAATGAGCCACGTAGTTCCTATTTAATGCTGTTTTCTT (1320)  
TAGTTTAGAAATACATAGACATTGTCTTTTATGAATTCTGATCATATTTAGTCATTTTG (1380)  
CCAAATGAGGGATTTGGTCAATGAGGGAATCCCTCAAAGCAATATCAGGTAAACCAAGT (1440)  
TGCTTTCCTCACTCCCTGTCATGAGACTTCAGTGTTAATGTTACAATACTTTTCGAAA (1500)  
GAATAAAATAGTTC (1514)

FIG. 7-2

TAGACCCAGAGAGGCTCAGCTGCACTCGCCCGGCTGGGAGAGCTGGGTGTGGGGAACATG (60)  
MET

GCCGGGCTCCGAGGCTCCTGCTGCTGCCCTGCTTCTGGCGCTGGCTCGCGGCTGCCT (120)  
ALAGLYPROPRDARGLEULEULEULEUPROLEULEULEUALALEUALAARGGLYLEUPRO

GGGGCCCTGGCTGCCAAGGTAAGAGCTTCCCAGGCTCTCCATGGCCACAGCTCCGGAGC (180)  
GLYALALEUALAALAGLN /

TCTCCCTGCCCATGAGCTCAGAGCCCCAGTCTGAGCCACAGCACAGCCCCAGGAAGC (240)

GGGTGGGTGTGAGCGGCTCCAGTGTCTGAGGACTCATTTAAGAGAAAGGAAAAGGT (300)

GGACCCGGTGGGAGTGGCGGGGCTGTCCAGGCAGGGCGCTGCTTGGGAGGAAGAAG (360)

CCCACAGTCTCGGAACACGAGGACAGCACCTCCCCAACACCACAGCCGGTGCCAGATC (420)

TGCTCCATGCCCCGTAAGGACCGTGTCTTTGGCGACATGTCAGCCCTGGGCTGTCTCAG (480)

GGCCCCACCATCCCCACCACTGTCCCCTGCAGGGAGGACATTCTCTGTCCTTCTGGCCAG (540)  
/

ACTGATGGTGACAGCCCAGGTCCTCCCAGAGGTGCAGCAGTCTCCCACAGTGCACGACTGT (600)  
GLUVALGLNGLNSERPROHISCYSTHRTHRVA

CCCCGTGGGAGCCTCCGTCAACATCACCTGTCCACCAGCGGGGGCCTGCGTGGGATCTA (660)  
LPROVALGLYALASERVALASNILETHRCYSSERTHRSERGLYGLYLEUARGGLYLETY  
---CHO---

CCTGAGGCACTCGGGCCACAGCCCAAGACATCATTTACTACGAGGACGGGTGGTGCC (720)  
RLEUARGGLNLEUGLYPROGLNPROGLNASPILEILETYRTYRGLUASPGLYVALVALPR

CACTACGGAACAGACGGTTCGGGGCCGATCGACTTCTCAGGGTCCCAGGACAACCTGAC (780)  
OTHRTHRASPARGARGPHEARGGLYARGILEASPPHESERGLYSERGLNASPASNLEUTH  
---CHO---

TATCACCATGACCGCCTGCAGCTGTGGACACTGGCACCTACACCTGCCAGGCCATCAC (840)  
RILETHRMETHISARGLEUGLNLEUSERASPTHRGLYTHRTYRTHRCYSLNALAILETH

GGAGGTCAATGTCTACGGCTCCGGCACCCCTGGTCTGGTGACAGAGGAACAGTCCCAAGG (900)  
RGLUVALASNVALTYRGLYSERGLYTHRLEUVALLEUVALTHRGLUGLUGLNSERGLNGL

ATGGCACAGATGCTCGGACGCCCCACCAAGGGCCTCTGCCCTCCCTGCCCCACCGACAGG (960)  
YTRPHISARGCYSSERASPALAPROPROARGALASERALEUVALPROALAPROPROTHRGL

CTCCGCCCTCCCTGACCCGACAGACAGCCTCTGCCCTCCCTGACCCGCCAGCAGCCTCTGC (1020)  
YSERALEULEUPROASPPROGLNTHRALASERALEUVALPROASPPROPROALAALASERAL

CCTCCCTGCGGCCCTGGCGGTGATCTCCTTCTCCTCGGGCTGGGCCTGGGGTGGCGTG (1080)  
ALEUVALALAALALEUALAVALILESERPHEULEUGLYLEUGLYLEUGLYVALALACY  
-----TM-----\*

FIG. 8-1

TGTGCTGGCGAGGACACAGATAAAGAACTGTGCTCGTGGCGGGATAAGAATTCGGCGGC (1140)  
 SVALLEUALAARGTHRGLNILELYSLYSLEUCYSSERTRPARGASPLYSASN SERALAAL  
 -----  
 ATGTGTGGTGTACGAGGACATGTCCGACAGCCGCTGCAACACGCTGTCC<sup>†</sup>CCCCAACCA (1200)  
 ACYSVALVALTYRGLUASPMETSERHIS SERARGCYSASN<sup>†</sup>THRLEUSERSERPROASNGL  
 GTACCAGTG<sup>†</sup>CCCCAGTGGG<sup>†</sup>CCCCTGCACG<sup>†</sup>CCCGCCTGT<sup>†</sup>GGTCCCCCAGCACCTTCCCT<sup>†</sup> (1260)  
 NTYRGLN<sup>†</sup>END  
 GCCCCACCATGCCCCCAC<sup>†</sup>CTGCCACAC<sup>†</sup>CTCACCTG<sup>†</sup>CTGTCTCC<sup>†</sup>CACGGCTGCA<sup>†</sup>G (1320)  
 CAGAGTTTG<sup>†</sup>AAGGGCCAG<sup>†</sup>CGTGCCAG<sup>†</sup>CTCAAGCAG<sup>†</sup>ACACAGGC<sup>†</sup>AGTGGCCAGG<sup>†</sup>C (1380)  
 CCCACGGTG<sup>†</sup>CTTCTCAGTGGACAATGATG<sup>†</sup>CTCCTCCGGGAAGCCTTCC<sup>†</sup>CTGCCAGCC<sup>†</sup>C (1440)  
 ACGCCGCCA<sup>†</sup>CCGGGAGGAAG<sup>†</sup>CCTGACTGT<sup>†</sup>CCTTTGGCTG<sup>†</sup>CATCTCCGA<sup>†</sup>CCATGGCCAAG<sup>†</sup> (1500)  
 GAGGGCTTT<sup>†</sup>CTGTGGGAT<sup>†</sup>GGCCTGGCA<sup>†</sup>CGCGCCCTC<sup>†</sup>CTGTCAGT<sup>†</sup>GCCGGCCAC<sup>†</sup>C (1560)  
 CACCAGCAG<sup>†</sup>CCCCCAACC<sup>†</sup>CCAGGCAGC<sup>†</sup>CCGCAGAGG<sup>†</sup>ACGGGAGGAG<sup>†</sup>ACCAGTCCCC<sup>†</sup>C (1620)  
 ACCCAGCCG<sup>†</sup>TACCAGAAAT<sup>†</sup>AAAGGCTTCTGTGCTTCAAAA<sup>†</sup>AAAAA (1665)  
 -----

FIG. 8-2

CCCAAATGTCTCAGAATGTATGTCCCAGAAACCTGTGGCTGCTTCAACCATTGACAGTTT (60)  
 METSERGLNASNVALCYSPROARGASNLEUTRPLEULEUGLNPROLEUTHRVALL  
 -29  
 TGCTGCTGCTGGCTTCTGCAGACAGTCAAGCTGCAGTCCCCAAAGGCTGTGCTGAAAC (120)  
 EULEULEULEUALASERALAASP SERGLNALAALAPROPROLYSALAVALLEULYSL  
 -1 +1  
 10 TTGAGCCCCCGTGGATCAACGTGCTCCAGGAGGACTCTGTGACTCTGACATGCCAGGGGG (180)  
 EUGLUPROPROTRP ILEASNVALLEUGLNGLUASPSERVALTHRLEUTHRCYSLNGLYA  
 30 CTCGCAGCCCTGAGAGCGACTCCATTGAGTGGTTCCACAATGGGAATCTCATTCCCACC (240)  
 LAARGSERPROGLUSERASPSERILEGLNTRPPHEHISASNGLYASNLEUILEPROTHR  
 50 ACACGCAGCCAGCTACAGGTTCAAGGCCAACAACATGACAGCGGGGAGTACACGTGCC (300)  
 ISTHRLNPROSERTYRARGPHELYSALAASNASNASNASPSERGLYGLUTYRTHRCYSG  
 ---CHO--- \*  
 70 AGACTGGCCAGACCAGCCTCAGCGACCCTGTGCATCTGACTGTGCTTTCCGAATGGCTGG (360)  
 LNTHRGLYGLNTHRSERLEUSERASPPROVALHISLEUTHRVALLLEUSERGLUTRPLEUV  
 90 TGCTCCAGACCCCTCACCTGGAGTTCAGGAGGGAGAAAACCATCATGCTGAGGTGCCACA (420)  
 ALLEUGLNTHRPROHISLEUGLUPHEGLNGLUGLYGLUTHRIEMETLEUARGCYSHISS  
 \*  
 110 GCTGGAAGGACAAGCCTCTGGTCAAGGTCAATTCTTCCAGAAATGGAAAATCCCAGAAAT (480)  
 ETRPLYSASPLYSPROLEUVALLYSVALTHRPHEPHEGLNASNGLYLYSSERGLNLYSP  
 130 TCTCCCGTTTGGATCCCACCTTCTCCATCCACAAGCAAACACAGTCAAGTGGTGATT (540)  
 HESERARGLEUASPPROTHRPHESERILEPROGLNALAASNHISSEHISSEHISSEGLYASPT  
 ---CHO---  
 150 ACCACTGCAAGGAAACATAGGCTACAGCTGTTCTCATCAAGCCTGTGACCATCACTG (600)  
 YRHISCYSTHRLYASNILEGLYTYRTHRLEUPHESERLYSERLYSPROVALTHRIETHRV  
 \*  
 170 TCCAAGTGCCAGCATGGGAGCTCTTCAACATGGGATCATTGTGGCTGTGGTCATTG (660)  
 ALGLNVALPROSERMETGLYSERSESRSESPROMETGLYILEILEVALALAVALLILEA  
 190 CGACTGCTGTAGCAGCCATTGTTGCTGCTGTAGTGGCCTTGATCTACTGCAGGAAAAAGC (720)  
 LATHRALAVALLAALAILEVALALAALAVALLAALALEUILETYRCYSARGLYSLYSA  
 -----TM-----\*-----  
 210 GGATTTAGCCAATTCCACTGATCCTGTGAAGGCTGCCAATTTGAGCCACCTGGACGTC (780)  
 RGILESERALAASNSETRHASPPOVALLYSALAALAGLNPHGLUPROPROGLYARGG  
 230 AAATGATTGCCATCAGAAAGAGACAACTTGAAGAAACCAACAATGACTATGAAACAGCTG (840)  
 LNMETILEALAILEARGLYSARGGLNLEUGLUGLUTHRASNASNASPTYRGLUTHRALAA  
 250 ACGGCGGCTACATGACTCTGAACCCAGGGCACCTACTGACGATGATAAAAACATCTACC (900)  
 SPGLYGLYTYRMETTHRLEUASNPROARGALAPROTHRASPPASPLYSASNILETYRL

FIG. 9-1



098544-043701

270 TGA CTCTTCCTCCCAACGA C CATGTCAACAGTAATAACTAAAGAGTAACGTTATGCCATG (960)  
EUTHRELEUPROPROASNASPHISVALASN SERASNENEND  
282  
TGGTCATACTCTCAGCTTGCTGAGTGGATGACAAAAAGAGGGGAATTGTTAAAGGAAAAT (1020)  
TTAAATGGAGACTGGAAAAATCCTGAGCAACAAAAACCACTGGCCCTTAGAAATAGCTT (1080)  
TAACTTTGCTTAACTACAACACAAGCAAACTTCACGGGGTCATACTACATACAAGCA (1140)  
TAAGCAAACTTAACTTGGATCATTTCTGGTAAATGCTTATGTTAGAAATAAGACAACCC (1200)  
CAGCCAATCACAAGCAGCCTACTAACATAATAATTAGGTGACTAGGGACTTTCTAAGAAGA (1260)  
TACCTACCCCAAAAAACAATTATGTAATTGAAAACCAACCGATTGCCTTTATTTTGCTT (1320)  
CCACATTTTCCAATAAATACTTGCTGTGACATTTTGCCTGGAACAATAAATTCAAT (1380)  
GAATTGCGCCTCAGATTTTCTTTAACAATCTTTTTTTTTTTTGACAGAGTCTCAATCTG (1440)  
TTACCCAGGCTGGAGTGCAGTGGTCTATCTTGGTCACTGCAAACCCGCTCCCAGGT (1500)  
TAAGCGATTCTCATGCCTCAGCCTCCAGTAGCTGGGATTAGAGGCATGTGCCATCATACT (1560)  
CCAGCTAATTTTTGTATTTTATTTTTTTTTTTTAGTAGAGACAGGGTTTCGCAATGTT (1620)  
GGCCAGGCCGATCTCGAACTTCTGGCCTCTAGCGATCTGCCCGCTCGGCTCCCAAAGT (1680)  
GCTGGGATGACCAGCATCAGCCCCAATGTCCAGCCTCTTTAACATCTTCTTCTATGCC (1740)  
CTCTCTGTGGATCCCTACTGCTGGTTTCTGCCTTCTCAATGCTGAGAACAAAATCACCTA (1800)  
TCACTGCTTATGCAGTCGGAAGCTCCAGAGAACAAGAGGCCAATTAACAGAACACAA (1860)  
TTAAGTCTCATTGTTTTGCCTTGGGATTGAGAAGAGAATTAGAGAGGTGAGGATCTGG (1920)  
TATTTCTGGACTAAATTCCTTGGGGAAGACGAAGGGATGCTGCAGTTCAAAAGAGA (1980)  
AGGACTCTTCAGAGTCATCTACCTGAGTCCCAAAGCTCCTGTCTGAAAGCCACAGAC (2040)  
AATATGGTCCCAAATGACTGACTGCACCTTCTGTGCCTCAGCCGTTCTTGACATCAAGAA (2100)  
TCTTCTGTTCCACATCCACACAGCCAATAACAATTAGTCAAACCACTGTTATTAACAGATG (2160)  
TAGCAACATGAGAAACGCTTATGTTACAGGTACATGAGAGCAATCATGTAAGTCTATAAT (2220)  
GACTTCAGAAATGTTAAAATAGACTAACCTCTAACAACAATTAAGTGAATTGTTCAA (2280)  
GGTGAAAAA (2290)

FIG. 9-2

```

1  AAAGACAAACTGCACCCCACTGAACTCCGCAGCTAGCATCCAAATCAGCCCTTGAGATTTGAGGCTTGGAGACTCAGGAGTTTIGAGAGC
91  AAAATGACAAACACCCAGAAATTACAGTAAATGGGACTTTCCTCCGGCAGAGCCCAATGAAAGGCCCTATTGCTATGCAATCTGGTCCAAAACCA
1  MetThrThrProArgAsnSerValAsnGlyThrPheProAlaGluProMetLysGlyProIleAlaMetGlnSerGlyProLysPro
    ---CHO---
181 CTCTTCAGGAGGATGCTCTTCACTGGTGGGCCCCACGCCAAAGCTTCTTCAIGAGGGAATCTAAGACTTTTGGGGGCTGTCCAGATTATGAAT
30  LeuPheArgArgMetSerSerLeuValGlyProThrGlnSerPhePheMetArgGluSerLysThrLeuGlyAlaValGlnIleMetAsn
    =====
271 GGGCTCTTCCACATTGCCCTGGGGGTCTTCTGATGATCCAGCAGGGAICTATGCACCCCATCTGTGTGACTGTGTGGTACCCCTCTCTGG
60  GlyLeuPheHisIleAlaLeuGlyGlyLeuLeuMetIleProAlaGlyIleTyrAlaProIleCysValThrValTrpTyrProLeuTrp
    =====
361 GGAGGCATTATGTATATTATTTCCGGATCACCTCCCTGGCAGCAACGGAGAAAACTCCAGGAAGTGTTTGGTCAAAGGAAATAATGATAATG
90  GlyGlyIleMetTyrIleIleSerGlySerLeuLeuAlaAlaThrGluLysAsnSerArgLysCysLeuValLysGlyLysMetIleMet
    =====
451 AATTCATTGAGCCTCTTTGCTGCCATTTCTGGAAATGATTCTTTCAATCATGGACATACTTAATAATTTCCCATTTTTTAAAAATG
120  AsnSerLeuSerLeuPheAlaAlaIleSerGlyMetIleLeuSerIleMetAspIleLeuAsnIleLysIleSerHisPheLeuLysMet
    =====
641 GAGAGTCTGAATTTTATTAGAGCTCACACACCATATATTAACATATACAACTGTGAACCAAGCTAATCCCTCTGAGAAATACTCCCCATCT
150  GluSerLeuAsnPheIleArgAlaHisThrProTyrIleAsnIleTyrAsnCysGluProAlaAsnProSerGluLysAsnSerProSer
    =====
631 ACCCAATACTGTTACAGCATACAATCTCTGTTCTTGGGCATTTTGTGAGTGATGCTGATCTTTGCCCTTCTTCCAGGAACCTTGTAATAGCT
180  ThrGlnTyrCysTyrSerIleGlnSerLeuPheLeuGlyIleLeuSerValMetLeuIlePheAlaPhePheGlnGluLeuValIleAla
    =====

```

FIG. 10A-1

721 GGCATCGTTGAGAAATGAATGGAAAAGAACGTGCTCCAGACCCAAATCTAACATAGTTCTCTGTCTCAGCAGAAAGAAAAAGAACAGACT  
210 GlyIleValGluAsnGluTrpLysArgThrCysSerArgProLysSerAsnIleValLeuLeuSerAlaGluGluLysLysGluGlnThr  
811 ATTGAAATAAAGAAGAAGTGGTGGCTAACTGAAACATCTTCCCAACCAAGAATGAAGAAGACATTGAAATTATTCCAATCCAAGAA  
240 IleGluIleLysGluGluValValGlyLeuThrGluThrSerSerGlnProLysAsnGluGluAspIleGluIleIleProIleGlnGlu  
901 GAGGAAGAAGAAGAACAGACGAACTTCCAGAACCTCCCCAAGATCAGGAATCCTCACCATAAGAAAATGACAGCTCTCCTTAAGTG  
270 GluGluGluGluThrGluThrAsnPheProGluProGlnAspGlnGluSerSerProIleGluAsnAspSerSerProEnd 297  
---CH0---

991 ATTTCTCTGTTTTCTGTTTCCCTTTTTTAAACATTAGTGTTTCATAGCTTCCAAGAGACATGCTGACTTTTTCATTCTTGAGGTACTCTGCA  
\*

1081 CATACGCACCACATCTCTATCTGGCCTTTGGCATGGAGTGACCATAGCTCCTTCTCTCTTACATTGAATGTAGAGAAATGTAGCCATTGTAG

1171 CAGCTTGTTGTCACGCTTCTTCTTTTGAGCAACTTTCCTTACACTGAAGAAAGCAGAATGAGTGCTTCAGAAATGTGATTTCCTACTAA

1261 CCTGTTCTGGATAGGCTTTTTTAGTATAGTATTTTTTTTTTGTCATTTTCTCCATCAGCAACCAGGGAGACTGCACCTGATGGAAAAGAT

1351 ATATGACTGCTTCATGACATTCCCTAAACTATCTTTTTTTTATCCACATCTACGTTTTTGGTGGAGTCCCCTTTTATCATCTCTTAAACA

1441 ATGATGCAAAAGGGCTTTAGAGCACAAATGGATCT 1474

FIG. 10A-2

TD 470" 41595860

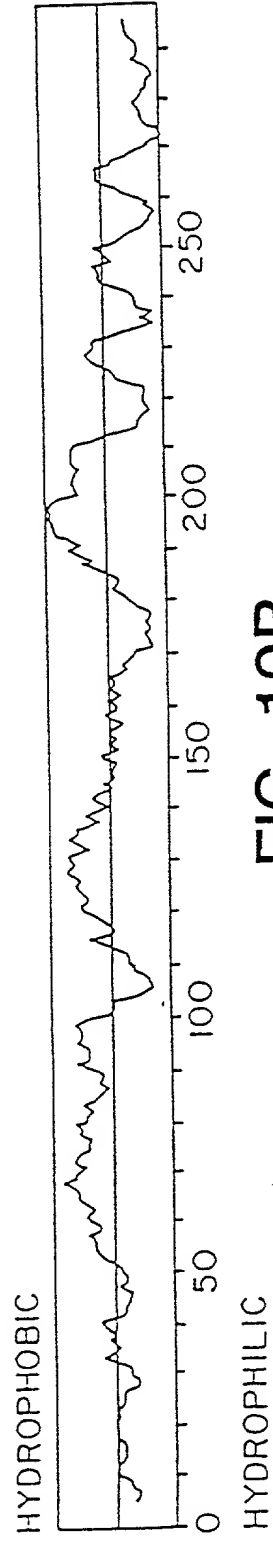


FIG. 10B

1 CTCAGCCTCGCTATGGCTCCAGCAGCCCCCGGCGCTGCGCCGACCTCCTGGTCTGCTCGGGGCTCTGTTCCCA  
MetAlaProSerSerProArgProAlaLeuProAlaLeuLeuValLeuLeuGlyAlaLeuPhePro  
(-25)  
GGACCTGGCAATGCCCAGACATCTGTGTCCCTCAAAAGTC  
GlyProGlyAsnAlaGlnThrSerValSerProSerLysVal  
(+11)  
121 ATCTGCCCGGGAGGCTCCGTGCTGGTGACATGCAGCACCTCCTGTGACCCCAAGTTGTTGGGCATAGAGACC  
IleLeuProArgGlyGlySerValLeuValThrCysSerThrSerCysAspGlnProLysLeuLeuGlyIleGluThr  
(+1)  
CCGTTGCCCTAAAAAGGAGTTGCTCCTGCCCTGGGAACAACCGG  
ProLeuProLysLysGluLeuLeuLeuProGlyAsnAsnArg  
(+51)  
241 AAGGTGTATGAAGTGAAGCAATGTGCAAGAAGATAGCCAACTGCTATTCAAACCTGCCCTGATGGGCAGTCAACA  
LysValTyrGluLeuSerAsnValGlnGluAspSerGlnProMetCysTyrSerAsnCysProAspGlyGlnSerThr  
GCTAAACCTTCTCACCGTGTACTGGACTCCAGAACGGGTG  
AlaLysThrPheLeuThrValTyrTrpThrProGluArgVal  
(+91)  
361 GAACTGGCACCCCTCCCTCTTGGCAGCCAGTGGGCAAGAACCTTACCCTACGCTGCCAGGTGGAGGTGGGGCACCC  
GluLeuAlaProLeuProSerTrpGlnProValGlyLysAsnLeuThrLeuArgCysGlnValGluGlyGlyAlaPro  
----CH0----  
CGGGCAACCTCACCGTGTGTCTCCGTGGGAGAGGAG  
ArgAlaAsnLeuThrValValLeuLeuArgGlyGluLysGlu  
-----(+131)  
481 CTGAAACGGGAGCCAGCTGTGGGGAGCCCCGCTGAGGTACGACCCACGGTGTGTGAGGAGATCACCATGGAGCC  
LeuLysArgGluProAlaValGlyGluProAlaGluValThrThrValLeuValArgArgAspHisGlyAla  
AATTTCTCGTGCCGCACTGAACCTGGACCTGCGGCCCCCAAGGG  
AsnPheSerCysArgThrGluLeuAspLeuArgProGlnGly  
----CH0----(+171)  
601 CTGGAGCTGTTTGAGAACACCTCGGCCCCCTACCAGCTCCAGACCTTTGTCTGCCAGCGACTCCCCCACAACCTTGTC  
LeuGluLeuPheGluAsnThrSerAlaProTyrGlnLeuGlnThrPheValLeuProAlaThrProProGlnLeuVal  
----CH0----  
AGCCCCCGGTCCTAGAGGTGGACACGCCAGGGGACCGTGGTC  
SerProArgValLeuGluValAspThrGlnGlyThrValVal  
(+211)

FIG. 11-1

721 TGTTCCCTGGACGGGCTGTTCCAGTCTCGGAGGCCAGGTCCACCTGGCACTGGGGACAGAGGTTGAACCCACACA  
CysSerLeuAspGlyLeuPheProValSerGluAlaGlnValHisLeuAlaLeuGlyAspGlnArgLeuAsnProThr  
GTCACCTATGGCAACGACTCCTTCTCGGCCAAGGCCTCAGTC  
ValThrTyrGlyAsnAspSerPheSerAlaLysAlaSerVal  
---CHO--- (+251)

841 AGTGTGACCGCAGAGGACGAGGGCACCCAGCGGCTGACGTGTGCAGTAATACTGGGGAACAGAGCCAGGAGACACTG  
SerValThrAlaGluAspGluGlyThrGlnArgLeuThrCysAlaValIleLeuGlyAsnGlnSerGlnGluThrLeu  
---CHO---  
CAGACAGTGACCATCTACAGCTTTCCGGCGCCCAACGTGATT  
GlnThrValThrIleTyrSerPheProAlaProAsnValIle  
---CHO--- (+291)

961 CTGACGAAGCCAGAGGTCTCAGAAGGGACCGAGGTGACAGTGAAGTGTGAGGCCACCCCTAGAGCCAAGGTGACGCTG  
LeuThrLysProGluValSerGluGlyThrGluValThrValLysCysGluAlaHisProArgAlaLysValThrLeu  
AATGGGGTTCCAGCCAGCCACTGGGCCCGAGGGCCCGAGCTC  
AsnGlyValProAlaGlnProLeuGlyProArgAlaGlnLeu  
---CHO--- (+331)

1081 CTGCTGAAGGCCACCCAGAGGACACACGGCGCAGCTTCTCTCTGCTCTGCAACCCCTGGAGGTGGCCGCGCAGCTTATA  
LeuLeuLysAlaThrProGluAspAsnGlyArgSerPheSerCysSerAlaThrLeuGluValAlaGlyGlnLeuIle  
CACAAAGAACCAAGACCCGGGAGCTTCGTGCTCTGTATGGCCCC  
HisLysAsnGlnThrArgGluLeuArgValLeuTyrGlyPro  
---CHO--- (+371)

1201 CGACTGGACGAGAGGGATTGTCCGGGAACTGGACGTGGCCAGAAATTCACAGCAGACTCCAATGTGCCAGGCTTGG  
ArgLeuAspGluArgAspCysProGlyAsnTrpThrTrpProGluAsnSerGlnGlnThrProMetCysGlnAlaTrp  
---CHO---  
GGGAACCCATTGCCCCGAGCTCAAGTGTCTAAAGGATGGCACT  
GlyAsnProLeuProGluLeuLysCysLeuLysAspGlyThr  
---CHO--- (+411)

1321 TTCCCACTGCCCATCGGGGAATCAGTGACTGTCACTCGAGATCTTGAGGGCACCTACCTCTGTGGGCCAGGAGCACT  
PheProLeuProIleGlyGluSerValThrValThrArgAspLeuGluGlyThrTyrLeuCysArgAlaArgSerThr  
CAAGGGGAGGTCACCCCGGAGGTGACCGTGAATGTGCTCTCC  
GlnGlyGluValThrArgGluValThrValAsnValLeuSer  
---CHO--- (+451)

FIG. 11-2

```

1441 CCCCAGTATGAGATTGTCTCATCTGTTGGTAGCAGCCGCGAGTCATAATGGGCACTGCAGGCCCTCAGCACGTACCTC
ProArgTyrGluIleValIleIleThrValValAlaAlaAlaValIleMetGlyThrAlaGlyLeuSerThrTyrLeu
-----TM-----
TATAACCGCCAGCGGAAGATCAAGAAATACAGACTACAAACAG
TyrAsnArgGlnArgLysIleLysLysTyrArgLeuGlnGln
(+491)
1561 GCCCCAAAAGGACCCCCCATGAAACCGAACACACACAGCCCTCCCTGAACCTATCCCGGGACAGGGCCTCTTCCT
AlaGlnLysGlyThrProMetLysProAsnThrGlnAlaThrProPro
(+507)
CGGCCTTCCCATATTGGTGGCAGTGGTGCCACACTGAACAGA

1681 GTGGAAGACATATGCCATGCGAGCTACACCTACCGGCCCTGGGACGCCGGAGGACAGGGCATTTGTCCTCAGTCAGATAC
1801 GGCCACGCACTCTGATCTGTAGTCACATGACTAAGCCAAAGAGGAAGG
AACAGCATTTGGGGCCATGGTACCTGCACACCTAAACACTA

```

FIG. 11-3

1 ..GGAGAGTC TGACCACCAT GCCACCTCCT CGCCTCCTCT TCTTCCTCCT  
51 CTTCTCACC CCCATGGAAG TCAGGCCCCA GGAACCTCTA GTGGTGAAGG  
101 TGGAAGAGGG AGATAACGCT GTGCTGCAGT GCCTCAAGGG GACCTCAGAT  
151 GGCCCCACTC AGCAGCTGAC CTGGTCTCGG GAGTCCCCGC TTAAACCCTT  
201 CTTAAAACTC AGCCTGGGGC TGCCAGGCCT GGAATCCAC ATGAGGCCCC  
251 TGGCCATCTG GCTTTTCATC TTCAACGTCT CTCAACAGAT GGGGGGCTTC  
301 TACCTGTGCC AGCCGGGGCC CCCCTCTGAG AAGGCCTGGC AGCCTGGCTG  
351 GACAGTCAAT GTGGAGGGCA GCGGGGAGCT GTTCCGGTGG AATGTTTCGG  
401 ACCTAGGTGG CCTGGGCTGT GGCCTGAAGA ACAGGTCCTC AGAGGGCCCC  
451 AGTCCCCCTT CCGGAAGCT CATGAGCCCC AAGCTGTATG TGTGGGCCAA  
501 AGACCGCCTT GAGATCTGGG AGGGAGAGCC TCCGTGTGTC CCACCGAGGG  
551 ACAGCCTGAA CCAGAGCCTC AGCCAGGACC TCACCATGGC CCCTGGCTCC  
601 AACTCTGGC TGTCTGTGG GGTACCCCTT GACTCTGTGT CCAGGGGCCC  
651 CCTCTCCTGG ACCCATGTGC ACCCAAGGG GCCTAAGTCA TTGCTGAGCC  
701 TAGAGCTGAA GGACGATCGC CCGGCCAGAG ATATGTGGGT AATGGAGAGC  
751 GGTCTGTTGT TGCCCCGGGC CACAGCTCAA GACGCTGGAA AGTATTATTG  
801 TCACCGTGGC AACCTGACCA TGTATTCCA CCTGGAGATC ACTGCTCGGC  
851 CAGTACTATG GCACTGGCTG CTGAGGACTG GTGGCTGGAA GGTCTCAGCT  
901 GTGACTTTGG CTTATCTGAT CTTCTGCCTG TGTCCCTTG TGGCATTCT  
951 TCATCTTCAA AGAGCCCTGG TCCTGAGGAG GAAAAGAAAG CGAATGACTG  
1001 ACCCCACCAG GAGATTCTTC AAAGTGACGC CTCCCCCAGG AAGCGGGCCC  
1051 CAGAACCAGT ACGGGAACGT GCTGTCTCTC CCCACACCCA CCTCAGGCCT  
1101 CGGACGCGCC CAGCGTTGGG CCGCAGGCCT GGGGGGCACT GCCCCGTCTT  
1151 ATGGAAACCC GAGCAGCGAC GTCCAGGCGG ATGGAGCCTT GGGGTCCCCG

FIG. 12-1



1201 AGCCGCCGGG AGTGGGCCCA GAAGAAGAGG AAGGGGAGGG CTATGAGGAA  
1251 CCTGACAGTG AGGAGGACTC CGAGTTCTAT GAGAACGACT CCAACCTTGG  
1301 GCAGGACCAG CTCTCCCAGG ATGGCAGCGG CTACGAGAAC CCTGAGGATG  
1351 AGCCCCTGGG TCCTGAGGAT GAAGACTCCT TCTCCAACGC TGAGTCTTAT  
1401 GAGAACGAGG ATGAAGAGCT GACCCAGCCG GTCGCCAGGA CAATGGACTT  
1451 CCTGAGCCCT CATGGGTCAG CCTGGGACCC CAGCCGGGAA GCAACCTCCC  
1501 TGGGGTCCCA GTCCTATGAG GATATGAGAG GAATCCTGTA TGCAGCCCCC  
1551 CAGCTCCGCT -CATTTCGGGG CCAGCCTGGA CCCAATCATG AGGAAGATGC  
1601 AGACTCTTAT GAGAACATGG ATAATCCCGA TGGGCCAGAC CCAGCCTGGG  
1651 GAGGAGGGGG CCGCATGGGC ACCTGGAGCA CCAGGTGATC CTCAGGTGGC  
1701 CAGCCTGGAT CTCCTCAAGT CCCCAAGATT CACACCTGAC TCTGAAATCT  
1751 GAAGACCTCG AGCAGATGAT GCCAACCTCT GGAGCAATGT TGCTTAGGAT  
1801 GTGTGCATGT GTGTAAGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT  
1851 ATACATGCCA GTGACACTTC CAGTCCCCTT TGTATTCCTT AAATAAACTC  
1901 AATGAGCTCT TCCAAAAAAA AAAA

FIG. 12-2

1 ACAAAGACAA ACTGCACCCA CTGAACTCCG CAGCTAGCAT CCAAATCAGC  
 51 CCTTGAGATT TGAGGCCTTG GAGACTCAGG AGTTTTGAGA GCAAAATGAC  
 101 AACACCCAGA AATTCAGTAA ATGGGACTTT CCCGGCAGAG CCAATGAAAG  
 151 GCCCTATTGC TATGCAATCT GGTCCAAAAC CACTCTTCAG GAGGATGTCT  
 201 TCACTGGTGG GCCCCACGCA AAGCTTCTTC ATGAGGGAAT CTAAGACTTT  
 251 GGGGGCTGTC CAGATTATGA ATGGGCTCTT CCACATTGCC CTGGGGGGTC  
 301 TTCTGATGAT CCCAGCAGGG ATCTATGCAC CCATCTGTGT GACTGTGTGG  
 351 TACCCTCTCT GGGGAGGCAT TATGTATATT ATTTCCGGAT CACTCCTGGC  
 401 AGCAACGGAG AAAA ACTCCA GGAAGTGTTT GGTCAAAGGA AAAATGATAA  
 451 TGAATTCATT GAGCCTCTTT GCTGCCATTT CTGGAATGAT TCTTTCAATC  
 501 ATGGACATAC TTAATATTAA AATTTCCCAT TTTTAAAAA TGGAGAGTCT  
 551 GAATTTTATT AGAGCTCACA CACCATATAT TAACATATAC AACTGTGAAC  
 601 CAGCTAATCC CTCTGAGAAA AACTCCCCAT CTACCCAATA CTGTTACAGC  
 651 ATACAATCTC TGTTCTTGGG CATTTTGTC A GTGATGCTGA TCTTTGCCTT  
 701 CTTCCAGGAA CTTGTAATAG CTGGCATCGT TGAGAATGAA TGGAAAAGAA  
 751 CGTGCTCCAG ACCCAAATCT AACATAGTTC TCCTGTCAGC ACAAGAAAAA  
 801 AAAGAACAGA CTATTGAAAT AAAAGAAGAA GTGGTTGGGC TAACTGAAAC  
 851 ATCTTCCCAA CCAAAGAATG AAGAAGACAT TGAAATTATT CCAATCCAAG  
 901 AAGAGGAAGA AGAAGAAACA GAGACGAACT TTCCAGAACC TCCCCAAGAT  
 951 CAGGAATCCT CACCAATAGA AAATGACAGC TCTCCTTAAG TGATTTCTTC  
 1001 TGTTTTCTGT TTCCTTTTTT AAACATTAGT GTTCATAGCT TCCAAGAGAC  
 1051 ATGCTGACTT TCATTTCTTG AGGTACTCTG CACATACGCA CCACATCTCT

FIG. 13-1

1101 ATCTGGCCTT TGCATGGAGT GACCATAGCT CCTTCTCTCT TACATTGAAT  
1151 GTAGAGAATG TAGCCATTGT AGCAGCTTGT GTTGTCACGC TTCTTCTTTT  
1201 GAGCAACTTT CTTACACTGA AGAAAGGCAG AATGAGTGCT TCAGAATGTG  
1251 ATTCCTACT AACCTGTTCC TTGGATAGGC TTTTGTAGTAT AGTATTTTTT  
1301 TTTGTCATTT TCTCCATCAG CAACCAGGGA GACTGCACCT GATGGAAAAG  
1351 ATATATGACT GCTTCATGAC ATTCCTAAAC TATCTTTTTT TTATTCCACA  
1401 TCTACGTTTT TGGTGGAGTC CCTTTTTATC ATCCTTAAAA CAATGATGCA  
1451 AAAGGGCTTT AGAGCACAAT GGATCT

FIG. 13-2

1 CCCAAATGTC TCAGAATGTA TGTCCCAGAA ACCTGTGGCT GCTTCAACCA  
 51 TTGACAGTTT TGCTGCTGCT GGCTTCTGCA GACAGTCAAG CTGCAGCTCC  
 101 CCCAAAGGCT GTGCTGAAAC TTGAGCCCCC GTGGATCAAC GTGCTCCAGG  
 151 AGGACTCTGT GACTCTGACA TGCCAGGGGG CTCGCAGCCC TGAGAGCGAC  
 201 TCCATTCACT GGTTCACAA TGGGAATCTC ATCCCACCC ACACGCAGCC  
 251 CAGCTACAGG TTCAAGGCCA ACAACAATGA CAGCGGGGAG TACACGTGCC  
 301 AGACTGGCCA GACCAGCCTC AGCGACCCTG TGCATCTGAC TGTGCTTTCC  
 351 GAATGGCTGG TGCTCCAGAC CCCTCACCTG GAGTTCAGG AGGGAGAAAC  
 401 CATCATGCTG AGGTGCCACA GCTGGAAGGA CAAGCCTCTG GTCAAGGTCA  
 451 CATTCTTCCA GAATGGAAAA TCCAGAAAT TCTCCCGTTT GGATCCCACC  
 501 TTCTCCATCC CACAAGCAAA CCACAGTCAC AGTGGTGATT ACCACTGCAC  
 551 AGGAAACATA GGCTACACGC TGTTCATC CAAGCCTGTG ACCATCACTG  
 601 TCCAAGTGCC CAGCATGGGC AGCTCTTCAC CAATGGGGAT CATTGTGGCT  
 651 GTGGTCATTG CGACTGCTGT AGCAGCCATT GTTGCTGCTG TAGTGGCCTT  
 701 GATCTACTGC AGGAAAAAGC GGATTTCAGC CAATTCCACT GATCCTGTGA  
 751 AGGCTGCCCA ATTTGAGCCA CCTGGACGTC AAATGATTGC CATCAGAAAG  
 801 AGACAACCTG AAGAAACCAA CAATGACTAT GAAACAGCTG ACGGCGGCTA  
 851 CATGACTCTG AACCCCAGGG CACCTACTGA CGATGATAAA AACATCTACC  
 901 TGA CTCTTCC TCCCAACGAC CATGTCAACA GTAATACTA AAGAGTAACG  
 951 TTATGCCATG TGGTCATACT CTCAGCTTGC TGAGTGGATG AAAAAAGAG  
 1001 GGGAAATTGT AAAGGAAAAT TTAAATGGAG ACTGGAAAAA TCCTGAGCAA  
 1051 AAAAAACCAC CTGGCCCTTA GAAATAGCTT TAACTTTGCT TAACTACAA  
 1101 ACACAAGCAA AACTTCACGG GGTCACTA CATACAAGCA TAAGCAAAAC  
 1151 TTA ACTTGA TCATTTCTGG TAAATGCTTA TGTTAGAAAT AAGACAACCC  
 1201 CAGCCAATCA CAAGCAGCCT ACTAACATAT AATTAGGTGA CTAGGGACTT  
 1251 TCTAAGAAGA TACCTACCCC CAAAAACAA TTATGTAATT GAAAACCAAC  
 1301 CGATTGCCTT TATTTTGCTT CCACATTTTC CCAATAAATA CTTGCCTGTG  
 1351 ACATTTTGCC ACTGGAACAC TAACTTCAT GAATTGCGCC TCAGATTTTT  
 1401 CCTTTAACAT CTTTTTTTTT TTTGACAGAG TCTCAATCTG TTACCCAGGC  
 1451 TGGAGTGCAG TGGTGCTATC TTGGCTCACT GCAAACCCGC CTCCCAGGT  
 1501 TAAGCGATTG TCATGCCTCA GCCTCCAGT AGCTGGGATT AGAGGCATGT  
 1551 GCCATCATAC CCAGCTAATT TTTGTATTTT TTATTTTTTT TTTTGTAGTAG  
 1601 AGACAGGGTT TCGCAATGTT GGCCAGGCCG ATCTCGAACT TCTGGCCTCT  
 1651 AGCGATCTGC CCGCCTCGGC CTCCCAAAGT GCTGGGATGA CCAGCATCAG

FIG. 15-1

1701 CCCCAATGTC CAGCCTCTTT AACATCTTCT TTCCTATGCC CTCTCTGTGG  
1751 ATCCCTACTG CTGGTTTCTG CCTTCTCCAT GCTGAGAACA AAATCACCTA  
1801 TTCACTGCTT ATGCAGTCGG AAGCTCCAGA AGAACAAAGA GCCCAATTAC  
1851 CAGAACCACA TTAAGTCTCC ATTGTTTTGC CTTGGGATTT GAGAAGAGAA  
1901 TTAGAGAGGT GAGGATCTGG TATTTCTGG ACTAAATTCC CCTTGGGGAA  
1951 GACGAAGGGA TGCTGCAGTT CAAAAGAGA AGGACTCTTC CAGAGTCATC  
2001 TACCTGAGTC CCAAAGCTCC CTGTCCTGAA AGCCACAGAC AATATGGTCC  
2051 CAAATGACTG ACTGCACCTT CTGTGCCTCA GCCGTTCTTG ACATCAAGAA  
2101 TCTTCTGTTT CACATCCACA CAGCCAATAC AATTAGTCAA ACCACTGTTA  
2151 TTAACAGATG TAGCAACATG AGAAACGCTT ATGTTACAGG TTACATGAGA  
2201 GCAATCATGT AAGTCTATAT GACTTCAGAA ATGTTAAAAT AGACTAACCT  
2251 CTAACAACAA ATTAAAAGTG ATTGTTTCAA GGTGAAAAAA

FIG. 15-2

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1  GCTGTGACTG CTGTGCTCTG GCGCCACTC GCTCCAGGGA GTGATGGGAA
51  TCCTGTCATT CTTACCTGTC CTTGCCACTG AGAGTGACTG GGCTGACTGc
101 AAGTCCCCC AGCCTTGGGG TCATATGCTT CTGTGGACAG CTGTGCTATC
151 CCTGGCTCCT GTTGCTGGGA CACCTGCAGC TCCCCAAAG GCTGTGCTGA
201 AACTCGAGCC CCAGTGGATC AACGTGCTCC AGGAGGACTC TGTGACTCTG
251 ACATGCCGGG GGA CTCACAG CCCTGAGAGC GACTCCATTC AGTGGTTCCA
301 CAATGGGAAT CTCATTCCCA CCCACACGCA GCCCAGCTAC AGGTTCAGG
351 CCAACAACAA TGACAGCGGG GAGTACACGT GCCAGACTGG CCAGACCAGC
401 CTCAGCGACC CTGTGCATCT GACTGTGCTT TCTGGTCAGT GGAGGAAGGC
451 CCCAGGGTGG ACCTGGGAGG GCCAGGACGG ATGAAATCTG CTTTCAGGCA
501 GAGGTTTGCA GGAAAGGGGG GTGGCCTGCT TACTGGGAAG TATCGCTGTG
551 AGTTGCCTCA GCACATATCA GTGGTTGTTT TTGCCTCAGT TCTGATTGAA
601 CAGAAGAAGG TTTCAAGGCC AAAACAGGC AGCCAAGTGT GAGAGAAGCA
651 GAAGGAAATC CCTACTGCAT AAAACCCATT TCCATTTTAA TGGCAGAATT
701 GAAAAGCACA GACCACAACT GAATCCTAGC CCTGGAAATG ACTCACTATA
751 CAACATGATG AATTCATTTA ACCCTTGAGT TTCCATTCTC TCACCTGCTC
801 CGTGGGGCAG TAACGCCTCC CTCAGAGGCT TCTGGTGAGA ATCAGTGTTT
851 CCCTGCCCCC GCCCCGCCCT CCATGCCCCT TCTCCACGTT CCACTGTGC
901 TAGGTGCTCT TCTCTGTCTT TCTCTCCAC CAGCCTGTGG GAAACCTGAG
951 ATGAAAGTCG TGTCTTACCC ATCTTTGTAT TTCCAGCATC TGAAACTGGG
1001 CAGAGCTTAA TAAATATTTT GCTGGAGAGG TTGATGATCT TACAAAGCTC
1051 CCATTGAAAG GTGGCTCTCT GTAAAGCAAA GTTACAATGA GATTGTGATG
1101 AACATTGTCC TTGTGGCTTT TCACTTAGTC CCCTCCCTTC ACCTGAAGAG
1151 CAAATTTTCC TCAAAAGTAC ACAGCAAACG AATGACCCAC TGGTGACACT
1201 GTTGCCTTTA GACCCTGCTG GAAAGAAGCT CCACATTTAT TAACATTCCC
1251 GAAGTAAATT TATCAGGTAG CATTATCAG GTAACATTG TTGCACATTC
1301 ATGACTTTTC TACTGTCCAC AAAGGCATAT GTCCTTATCA TATGCGGACT
1351 CCTCGGTCAC ACTGGATTCT TCCTTCCCTC CTCGACATGG AAGAGATGGC
1401 ATCTTAGGGT CTCTTGTTT CTTCTGCAG AGGCCTGTCG GGCAGGAAAA
1451 GGCTGCAGCT GCCTTCCTGG GAGAAGGAGG AGATGAGTGT ATCCTGAACA
1501 CCTATTATGT GCTAGGGGCT ATTGTAGATA CATGACACTA TCATGCTCAT
1551 TTTACGAAT GAGGAACTG AGGCTCAGAA GACTTAAATT ATTTGCCAA
1601 GAGTTATAAA TGACAGAGCC AGCATTAGAG TCCAGGACTG TCTGATTCA
1651 GACCTAAGCT GTTCCCTCTG CACATCGTGT CCCACCAGTA AGGAAGATCT

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FIG. 16-1

1701 GGGTCTCAGA GCTGAGCCAA GACCTCCCGG GTCCTCTGCG GTTTTTTGTG  
1751 TCTTTCAGAG TGGCTGGTGC TCCAGACCCC TCACCTGGAG TTCCAGGAGG  
1801 GAGAAACCAT CGTGCTGAGG TGCCACAGCT GGAAGGACAA GCCTCTGGTC  
1851 AAGGTCACAT TCTTCCAGAA TGGAAAATCC AAGAAATTTT CCCGTTCCGA  
1901 TCCCAACTTC TCCATCCCAC AAGCAAACCA CAGTCACAGT GGTGATTACC  
1951 ACTGCACAGG AAACATAGGC TACACGCTGT ACTCATCCAA GCCTGTGACC  
2001 ATCACTGTCC AAGCTCCCAG CTCTTCACCG ATGGGGATCA TTGTGGCTGT  
2051 GGTCACCTGGG ATTGCTGTAG CGGCCATTGT TGCTGCTGTA GTGGCCTTGA  
2101 TCTACTGCAG GAAAAAGCGG ATTCAGGTT TGTAGCTCCT CCCGGTCCCT  
2151 TTTGTTATCA GTTCCACTT T

FIG. 16-2

1 GCCTCGCTCG GGGCCCCAGT GGTCTGCCG CCTGGTCTCA CCTCGCCATG  
 51 GTTCGTCTGC CTCTGCAGTG CGTCCTCTGG GGCTGCTTGC TGACCGCTGT  
 101 CCATCCAGAA CCACCCACTG CATGCAGAGA AAAACAGTAC CTAATAAACA  
 151 GTCAGTGCTG TTCTTGTGTC CAGCCAGGAC AGAACTGGT GAGTGACTGC  
 201 ACAGAGTTCA CTGAAACGGA ATGCCTTCCT TGCGGTGAAA GCGAATTCCT  
 251 AGACACCTGG AACAGAGAGA CACACTGCCA CCAGCACAAA TACTGCGACC  
 301 CCAACCTAGG GCTTCGGGTC CAGCAGAAGG GCACCTCAGA AACAGACACC  
 351 ATCTGCACCT GTGAAGAAGG CTGGCACTGT ACGAGTGAGG CCTGTGAGAG  
 401 CTGTGTCCTG CACCGCTCAT GCTCGCCCGG CTTTGGGGTC AAGCAGATTG  
 451 CTACAGGGGT TTCTGATACC ATCTGCGAGC CCTGCCCAGT CGGCTTCTTC  
 501 TCCAATGTGT CATCTGCTTT CGAAAAATGT CACCCTTGGA CAAGCTGTGA  
 551 GACCAAAGAC CTGGTTGTGC AACAGGCAGGC ACAAACAAGA CTGATGTTGT  
 601 CTGTGGTCCC CAGGATCGGC TGAGAGCCCT GGTGGTGATC CCCATCATCT  
 651 TCGGGATCCT GTTTGCCATC CTCTTGGTGC TGGTCTTTAT CAAAAAGGTG  
 701 GCCAAGAAGC CAACCAATAA GGCCCCCAC CCCAAGCAGG AACCCAGGA  
 751 GATCAATTTT CCCGACGATC TTCCTGGCTC CAACACTGCT GCTCCAGTGC  
 801 AGGAGACTTT ACATGGATGC CAACCGGTCA CCCAGGAGGA TGGCAAAGAG  
 851 AGTCGCATCT CAGTGCAGGA GAGACAGTGA GGCTGCACCC ACCCAGGAGT  
 901 GTGGCCACGT GGGCAAACAG GCAGTTGGCC AGAGAGCCTG GTGCTGCTGC  
 951 TGCAGGGGTG CAGGCAGAAG CGGGGAGCTA TGCCCAGTCA GTGCCAGCCC  
 CTC

FIG. 17